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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/029,677

DATE: 05/16/2002
TIME: 13:22:07

Input Set : A:\PTO.VSK.txt
Output Set: N:\CRF3\05162002\J029677.raw

```
 3 <110> APPLICANT: Westphal, Ryan S.
 4        Feder, John N.
 5        Ramanathan, Chandra S.
 6        Mintier, Gabriel A.
 8 <120> TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND POLYPEPTIDES FOR A HUMAN CATION
CHANNEL
 9        POLYPEPTIDE
11 <130> FILE REFERENCE: D0187NP
W--> 12 <140> CURRENT APPLICATION NUMBER: 10/029,677
C--> 13 <141> CURRENT FILING DATE: 2002-05-06
15 <150> PRIOR APPLICATION NUMBER: US 60/257,865
16 <151> PRIOR FILING DATE: 2000-12-21
18 <160> NUMBER OF SEQ ID NOS: 24
20 <170> SOFTWARE: PatentIn version 3.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 2186
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (20)..(2011)
31 <220> FEATURE:
32 <221> NAME/KEY: misc_feature
33 <222> LOCATION: (2150)..(2150)
34 <223> OTHER INFORMATION: wherein "n" equals A, C, G, or T.
37 <400> SEQUENCE: 1
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39                       Met Thr Glu Lys Thr Asn Gly Val Lys Ser Ser
                          1           5                   10
40 cca gcc aat aat cac aac cat cat gca cct cct gcc atc aag gcc aat        100
42 Pro Ala Asn Asn His Asn His His Ala Pro Pro Ala Ile Lys Ala Asn
43                15                  20                  25
44 ggc aaa gat gac cac agg aca agc agc agg cca cac tct gca gct gac        148
46 Gly Lys Asp Asp His Arg Thr Ser Ser Arg Pro His Ser Ala Ala Asp
47        30                  35                  40
48 gat gac acc tcc tca gaa ctg cag agg ctg gca gac gtg gat gcc cca        196
50 Asp Asp Thr Ser Ser Glu Leu Gln Arg Leu Ala Asp Val Asp Ala Pro
51        45                  50                  55
52 cag cag gga agg agt ggc ttc cgc agg ata gtt cgc ctg gtg ggg atc        244
54 Gln Gln Gly Arg Ser Gly Phe Arg Arg Ile Val Arg Leu Val Gly Ile
55 60                  65                  70                  75
56 atc aga gaa tgg gcc aac aag aat ttc cga gag gag gaa cct agg cct        292
58 Ile Arg Glu Trp Ala Asn Lys Asn Phe Arg Glu Glu Glu Pro Arg Pro
59                80                  85                  90
60
```

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```
62 gac tca ttc ctc gag cgt ttt cgt ggg cct gaa ctc cag act gtg acc     340
63 Asp Ser Phe Leu Glu Arg Phe Arg Gly Pro Glu Leu Gln Thr Val Thr
64          95                      100                 105
66 aca cag gag ggg gat ggc aaa ggc gac aag gat ggc gag gac aaa ggc     388
67 Thr Gln Glu Gly Asp Gly Lys Gly Asp Lys Asp Gly Glu Asp Lys Gly
68          110                     115                 120
70 acc aag aag aaa ttt gaa cta ttt gtc ttg gac cca gct ggg gat ttg     436
71 Thr Lys Lys Lys Phe Glu Leu Phe Val Leu Asp Pro Ala Gly Asp Leu
72          125                     130                 135
74 tac tac tgc tgg cta ttt gtc att gcc atg ccc gtc ctt tac aac tgg     484
75 Tyr Tyr Cys Trp Leu Phe Val Ile Ala Met Pro Val Leu Tyr Asn Trp
76 140                         145                 150             155
78 tgc ctg ctg gtg gcc aga gcc tgc ttc agt gac cta cag aaa ggc tac     532
79 Cys Leu Leu Val Ala Arg Ala Cys Phe Ser Asp Leu Gln Lys Gly Tyr
80                          160                 165                 170
82 tac ctg gtg tgg ctg gtg ctg gat tat gtc tca gat gtg gtc tac att     580
83 Tyr Leu Val Trp Leu Val Leu Asp Tyr Val Ser Asp Val Val Tyr Ile
84                      175                 180                 185
86 gcg gac ctc ttc atc cga ttg cgc aca ggt ttc ctg gag cag ggg ctg     628
87 Ala Asp Leu Phe Ile Arg Leu Arg Thr Gly Phe Leu Glu Gln Gly Leu
88          190                     195                 200
90 ctg gtc aaa gat acc aag aaa ctg cga gac aac tac atc cac acc ctg     676
91 Leu Val Lys Asp Thr Lys Lys Leu Arg Asp Asn Tyr Ile His Thr Leu
92          205                     210                 215
94 cag ttc aag ctg gat gtg gct tcc atc atc ccc act gac ctg atc tat     724
95 Gln Phe Lys Leu Asp Val Ala Ser Ile Ile Pro Thr Asp Leu Ile Tyr
96 220                         225                 230             235
98 ttt gct gtg gac atc cac agc cct gag gtg cgc ttc aac cgc ctg ctg     772
99 Phe Ala Val Asp Ile His Ser Pro Glu Val Arg Phe Asn Arg Leu Leu
100                         240                 245                 250
102 cac ttt gcc cgc atg ttt gag ttc ttt gac cgg aca gag aca cgc acc     820
103 His Phe Ala Arg Met Phe Glu Phe Phe Asp Arg Thr Glu Thr Arg Thr
104                         255                 260                 265
106 aac tac cct aac atc ttc cgc atc agc aac ctt gtc ctc tac atc ttg     868
107 Asn Tyr Pro Asn Ile Phe Arg Ile Ser Asn Leu Val Leu Tyr Ile Leu
108                         270                 275                 280
110 gtc atc atc cac tgg aat gcc tgc atc tat tat gcc atc tcc aaa tcc     916
111 Val Ile Ile His Trp Asn Ala Cys Ile Tyr Tyr Ala Ile Ser Lys Ser
112          285                     290                 295
114 ata ggc ttt ggg gtc gac acc tgg gtt tac cca aac atc act gac cct     964
115 Ile Gly Phe Gly Val Asp Thr Trp Val Tyr Pro Asn Ile Thr Asp Pro
116 300                         305                 310             315
118 gag tat ggc tac ctg gct agg gaa tac atc tat tgc ctt tac tgg tcc    1012
119 Glu Tyr Gly Tyr Leu Ala Arg Glu Tyr Ile Tyr Cys Leu Tyr Trp Ser
120                         320                 325                 330
122 aca ctg act ctc act acc att ggg gag aca cca ccc cct gta aag gat    1060
123 Thr Leu Thr Leu Thr Thr Ile Gly Glu Thr Pro Pro Pro Val Lys Asp
124                      335                 340                 345
126 gag gag tac cta ttt gtc atc ttt gac ttc ctg att ggc gtc ctc atc    1108
```

```
127 Glu Glu Tyr Leu Phe Val Ile Phe Asp Phe Leu Ile Gly Val Leu Ile
128         350                 355             360
130 ttt gcc acc atc gtg gga aat gtg ggc tcc atg atc tcc aac atg aat      1156
131 Phe Ala Thr Ile Val Gly Asn Val Gly Ser Met Ile Ser Asn Met Asn
132     365                 370             375
134 gcc acc cgg gca gag ttc cag gct aag atc gat gcc gtg aaa cac tac      1204
135 Ala Thr Arg Ala Glu Phe Gln Ala Lys Ile Asp Ala Val Lys His Tyr
136 380                 385             390                 395
138 atg cag ttc cga aag gtc agc aag ggg atg gaa gcc aag gtc att agg      1252
139 Met Gln Phe Arg Lys Val Ser Lys Gly Met Glu Ala Lys Val Ile Arg
140                 400             405                 410
142 tgg ttt gac tac ttg tgg acc aat aag aag aca gtg gat gag cga gaa      1300
143 Trp Phe Asp Tyr Leu Trp Thr Asn Lys Lys Thr Val Asp Glu Arg Glu
144                 415             420             425
146 att ctc aag aat ctg cca gcc aag ctc agg gct gag ata gcc acc aat      1348
147 Ile Leu Lys Asn Leu Pro Ala Lys Leu Arg Ala Glu Ile Ala Thr Asn
148             430             435             440
150 gtc cac ttg tcc aca ctc aag aaa gtg cgc atc ttc cat gat tgt gag      1396
151 Val His Leu Ser Thr Leu Lys Lys Val Arg Ile Phe His Asp Cys Glu
152     445             450             455
154 gct ggc ctg ctg gta gag ctg gta ctg aaa ctc cgt cct cag gtc ttc      1444
155 Ala Gly Leu Leu Val Glu Leu Val Leu Lys Leu Arg Pro Gln Val Phe
156 460             465             470                 475
158 agt cct ggg gat tac att tgc cgc aaa ggg gac atc ggc aag gag atg      1492
159 Ser Pro Gly Asp Tyr Ile Cys Arg Lys Gly Asp Ile Gly Lys Glu Met
160             480             485             490
162 tac atc att aag gag ggc aaa ctg gca gtg gtg gct gat gat ggt gtg      1540
163 Tyr Ile Ile Lys Glu Gly Lys Leu Ala Val Val Ala Asp Asp Gly Val
164             495             500             505
166 act cag tat gct ctg ctg tcg gct gga agc tgc ttt ggc gag atc agt      1588
167 Thr Gln Tyr Ala Leu Leu Ser Ala Gly Ser Cys Phe Gly Glu Ile Ser
168         510             515             520
170 atc ctt aac att aag ggc agt aaa atg ggc aat cga cgc aca gct aat      1636
171 Ile Leu Asn Ile Lys Gly Ser Lys Met Gly Asn Arg Arg Thr Ala Asn
172     525             530             535
174 atc cgc agc ctg ggc tac tca gat ctc ttc tgc ttg tcc aag gat gat      1684
175 Ile Arg Ser Leu Gly Tyr Ser Asp Leu Phe Cys Leu Ser Lys Asp Asp
176 540             545             550                 555
178 ctt atg gaa gct gtg act gag tac cct gat gcc aag aaa gtc cta gaa      1732
179 Leu Met Glu Ala Val Thr Glu Tyr Pro Asp Ala Lys Lys Val Leu Glu
180                 560             565             570
182 gag agg ggt cgg gag atc ctc atg aag gag gga ctg ctg gat gag aac      1780
183 Glu Arg Gly Arg Glu Ile Leu Met Lys Glu Gly Leu Leu Asp Glu Asn
184             575             580             585
186 gaa gtg gca acc agc atg gag gtc gac gtg cag gag aag cta ggg cag      1828
187 Glu Val Ala Thr Ser Met Glu Val Asp Val Gln Glu Lys Leu Gly Gln
188     590                 595             600
190 ctg gag acc aac atg gaa acc ttg tac act cgc ttt ggc cgc ctg ctg      1876
191 Leu Glu Thr Asn Met Glu Thr Leu Tyr Thr Arg Phe Gly Arg Leu Leu
```

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192      605                    610                 615
194 gct gag tac acg ggg gcc cag cag aag ctc aag cag cgc atc aca gtt    1924
195 Ala Glu Tyr Thr Gly Ala Gln Gln Lys Leu Lys Gln Arg Ile Thr Val
196 620                    625                 630                 635
198 ctg gaa acc aag atg aaa cag aac aat gaa gat gac tac ctg tct gat    1972
199 Leu Glu Thr Lys Met Lys Gln Asn Asn Glu Asp Asp Tyr Leu Ser Asp
200                    640                 645                 650
202 ggg atg aac agc cct gag ctg gct gct gct gac gag cca taagacctgg    2021
203 Gly Met Asn Ser Pro Glu Leu Ala Ala Ala Asp Glu Pro
204                    655                 660
206 ggcccaactg cctctccagc attggccttg gccttgatcc cagaagctag aggagctatt    2081
208 tagatctccg gatttacatg cattaccctc atgttccctg aattctccca aaagtctctc    2141
210 tgaccctgng tttttggcct aaacatccaa gattccgcct cggat                    2186
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W-->

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213 <210> SEQ ID NO: 2
214 <211> LENGTH: 664
215 <212> TYPE: PRT
216 <213> ORGANISM: Homo sapiens
219 <400> SEQUENCE: 2
221 Met Thr Glu Lys Thr Asn Gly Val Lys Ser Ser Pro Ala Asn Asn His
222 1               5                10                  15
225 Asn His His Ala Pro Pro Ala Ile Lys Ala Asn Gly Lys Asp Asp His
226              20              25               30
229 Arg Thr Ser Ser Arg Pro His Ser Ala Ala Asp Asp Asp Thr Ser Ser
230        35               40              45
233 Glu Leu Gln Arg Leu Ala Asp Val Asp Ala Pro Gln Gln Gly Arg Ser
234     50               55              60
237 Gly Phe Arg Arg Ile Val Arg Leu Val Gly Ile Ile Arg Glu Trp Ala
238 65               70               75               80
241 Asn Lys Asn Phe Arg Glu Glu Glu Pro Arg Pro Asp Ser Phe Leu Glu
242              85               90               95
245 Arg Phe Arg Gly Pro Glu Leu Gln Thr Val Thr Thr Gln Glu Gly Asp
246        100              105              110
249 Gly Lys Gly Asp Lys Asp Gly Glu Asp Lys Gly Thr Lys Lys Lys Phe
250     115              120              125
253 Glu Leu Phe Val Leu Asp Pro Ala Gly Asp Leu Tyr Tyr Cys Trp Leu
254    130              135              140
257 Phe Val Ile Ala Met Pro Val Leu Tyr Asn Trp Cys Leu Leu Val Ala
258 145              150              155              160
261 Arg Ala Cys Phe Ser Asp Leu Gln Lys Gly Tyr Tyr Leu Val Trp Leu
262              165              170              175
265 Val Leu Asp Tyr Val Ser Asp Val Val Tyr Ile Ala Asp Leu Phe Ile
266        180              185              190
269 Arg Leu Arg Thr Gly Phe Leu Glu Gln Gly Leu Leu Val Lys Asp Thr
270     195              200              205
273 Lys Lys Leu Arg Asp Asn Tyr Ile His Thr Leu Gln Phe Lys Leu Asp
274    210              215              220
277 Val Ala Ser Ile Ile Pro Thr Asp Leu Ile Tyr Phe Ala Val Asp Ile
278 225              230              235              240
281 His Ser Pro Glu Val Arg Phe Asn Arg Leu Leu His Phe Ala Arg Met
```

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```
                         245                    250                255
282
285  Phe Glu Phe Phe Asp Arg Thr Glu Thr Arg Thr Asn Tyr Pro Asn Ile
286                 260                265                270
289  Phe Arg Ile Ser Asn Leu Val Leu Tyr Ile Leu Val Ile Ile His Trp
290        275                280                285
293  Asn Ala Cys Ile Tyr Tyr Ala Ile Ser Lys Ser Ile Gly Phe Gly Val
294        290                295                300
297  Asp Thr Trp Val Tyr Pro Asn Ile Thr Asp Pro Glu Tyr Gly Tyr Leu
298 305                310                315                320
301  Ala Arg Glu Tyr Ile Tyr Cys Leu Tyr Trp Ser Thr Leu Thr Leu Thr
302                 325                330                335
305  Thr Ile Gly Glu Thr Pro Pro Pro Val Lys Asp Glu Glu Tyr Leu Phe
306                 340                345                350
309  Val Ile Phe Asp Phe Leu Ile Gly Val Leu Ile Phe Ala Thr Ile Val
310        355                360                365
313  Gly Asn Val Gly Ser Met Ile Ser Asn Met Asn Ala Thr Arg Ala Glu
314        370                375                380
317  Phe Gln Ala Lys Ile Asp Ala Val Lys His Tyr Met Gln Phe Arg Lys
318 385                390                395                400
321  Val Ser Lys Gly Met Glu Ala Lys Val Ile Arg Trp Phe Asp Tyr Leu
322                 405                410                415
325  Trp Thr Asn Lys Lys Thr Val Asp Glu Arg Glu Ile Leu Lys Asn Leu
326                 420                425                430
329  Pro Ala Lys Leu Arg Ala Glu Ile Ala Thr Asn Val His Leu Ser Thr
330        435                440                445
333  Leu Lys Lys Val Arg Ile Phe His Asp Cys Glu Ala Gly Leu Leu Val
334        450                455                460
337  Glu Leu Val Leu Lys Leu Arg Pro Gln Val Phe Ser Pro Gly Asp Tyr
338 465                470                475                480
341  Ile Cys Arg Lys Gly Asp Ile Gly Lys Glu Met Tyr Ile Ile Lys Glu
342                 485                490                495
345  Gly Lys Leu Ala Val Val Ala Asp Asp Gly Val Thr Gln Tyr Ala Leu
346        500                505                510
349  Leu Ser Ala Gly Ser Cys Phe Gly Glu Ile Ser Ile Leu Asn Ile Lys
350        515                520                525
353  Gly Ser Lys Met Gly Asn Arg Arg Thr Ala Asn Ile Arg Ser Leu Gly
354        530                535                540
357  Tyr Ser Asp Leu Phe Cys Leu Ser Lys Asp Asp Leu Met Glu Ala Val
358 545                550                555                560
361  Thr Glu Tyr Pro Asp Ala Lys Lys Val Leu Glu Glu Arg Gly Arg Glu
362                 565                570                575
365  Ile Leu Met Lys Glu Gly Leu Leu Asp Glu Asn Glu Val Ala Thr Ser
366                 580                585                590
369  Met Glu Val Asp Val Gln Glu Lys Leu Gly Gln Leu Glu Thr Asn Met
370        595                600                605
373  Glu Thr Leu Tyr Thr Arg Phe Gly Arg Leu Leu Ala Glu Tyr Thr Gly
374 610                615                620
377  Ala Gln Gln Lys Leu Lys Gln Arg Ile Thr Val Leu Glu Thr Lys Met
378 625                630                635                640
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 05/16/2002
PATENT APPLICATION: US/10/029,677   TIME: 13:22:08

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<u>Please Note:</u>
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 2150

VERIFICATION SUMMARY
PATENT APPLICATION: **US/10/029,677**

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Input Set : **A:\PTO.VSK.txt**
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L:12 M:283 W: Missing Blank Line separator, <140> field identifier
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:210 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:2141